

FIG. 1A

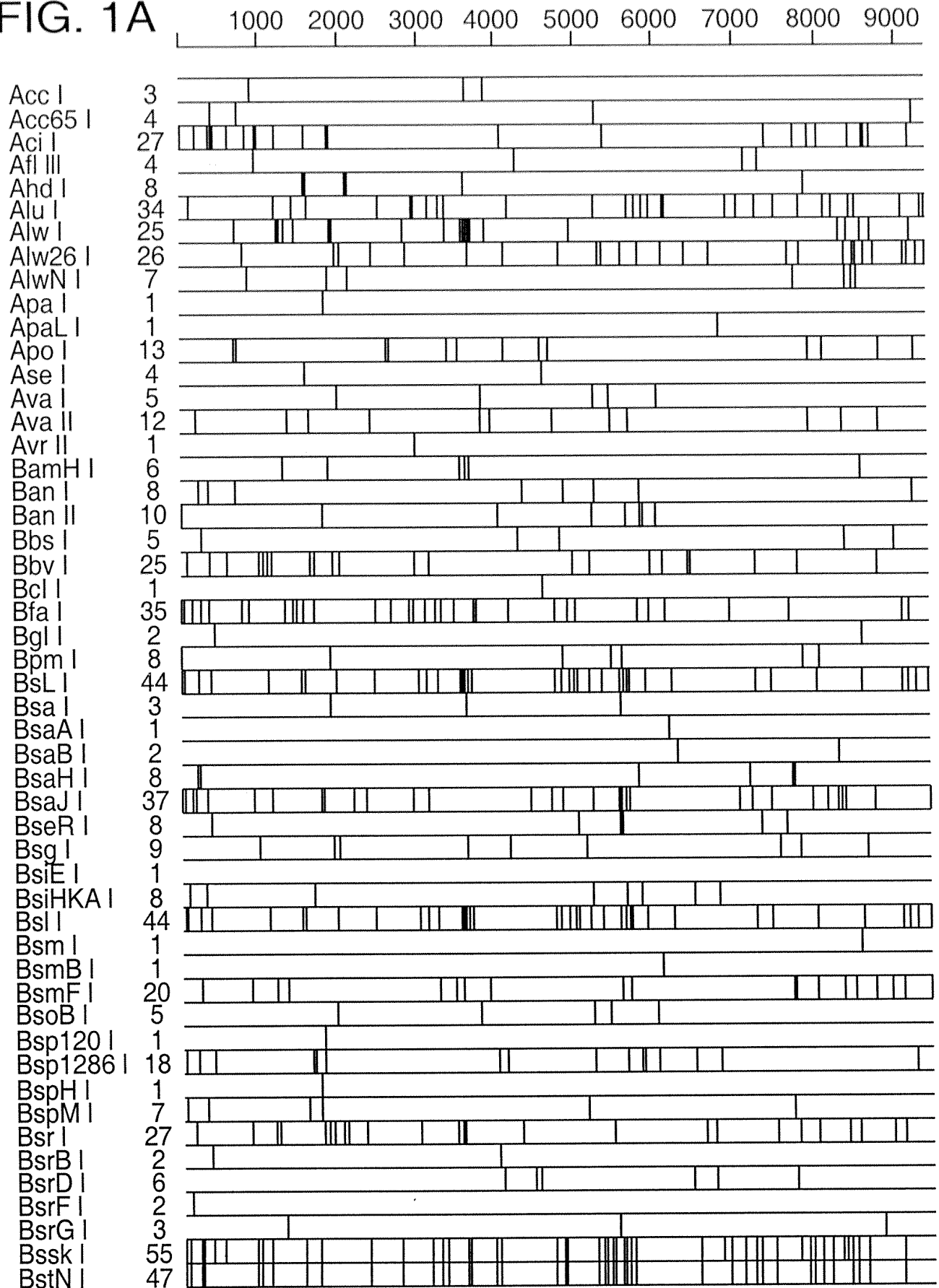


FIG. 1B

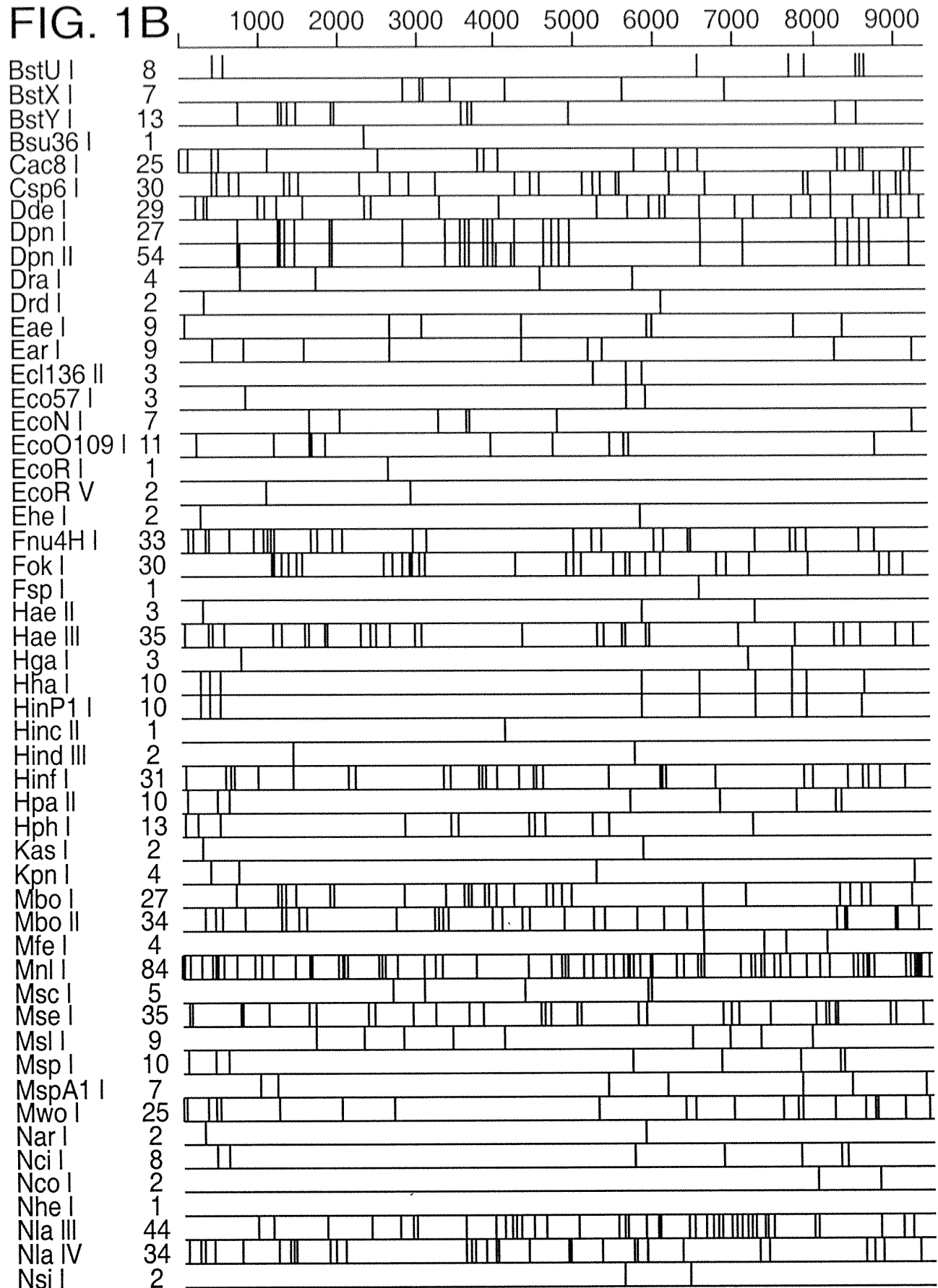


FIG. 1C

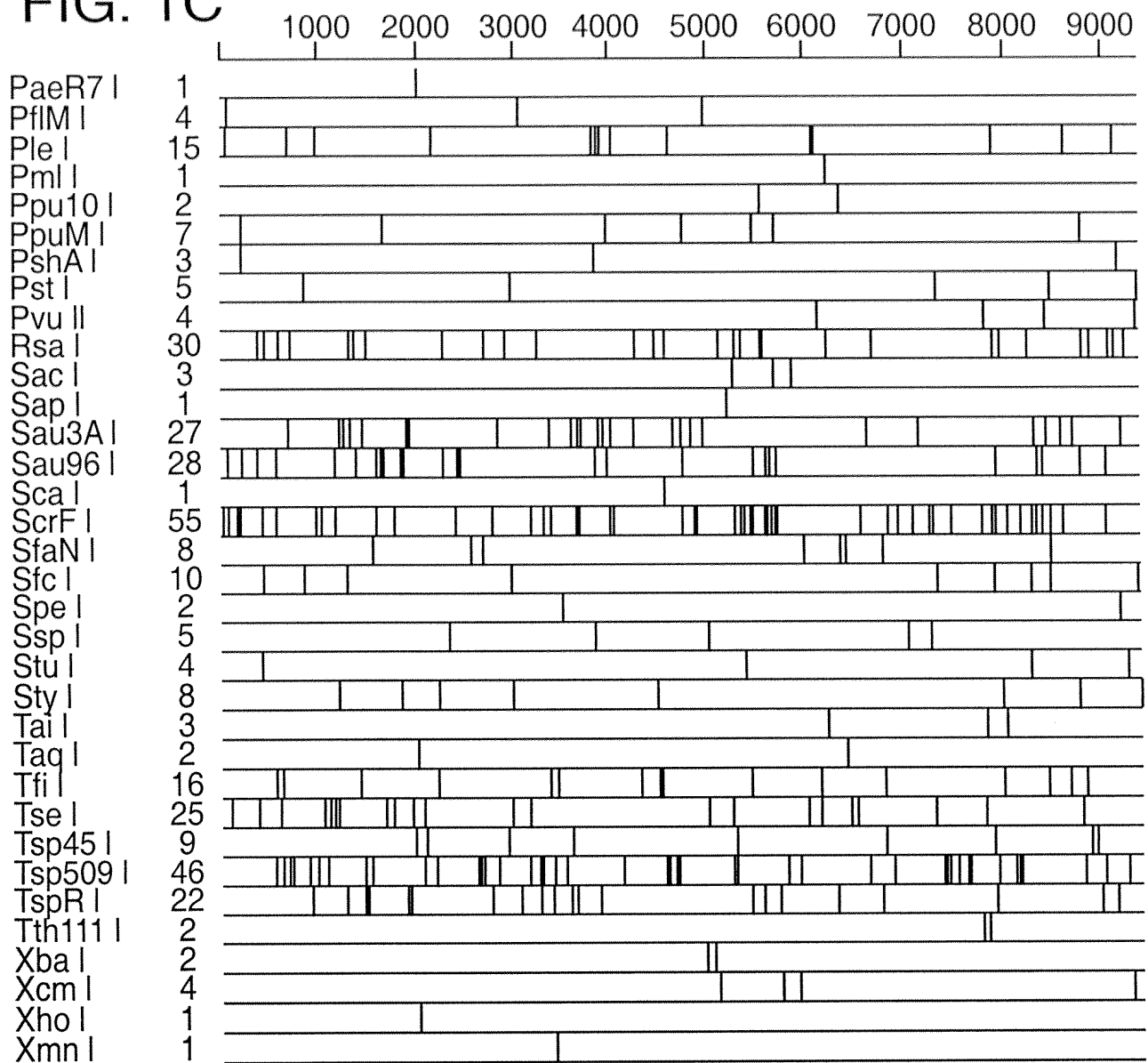


FIG. 2A

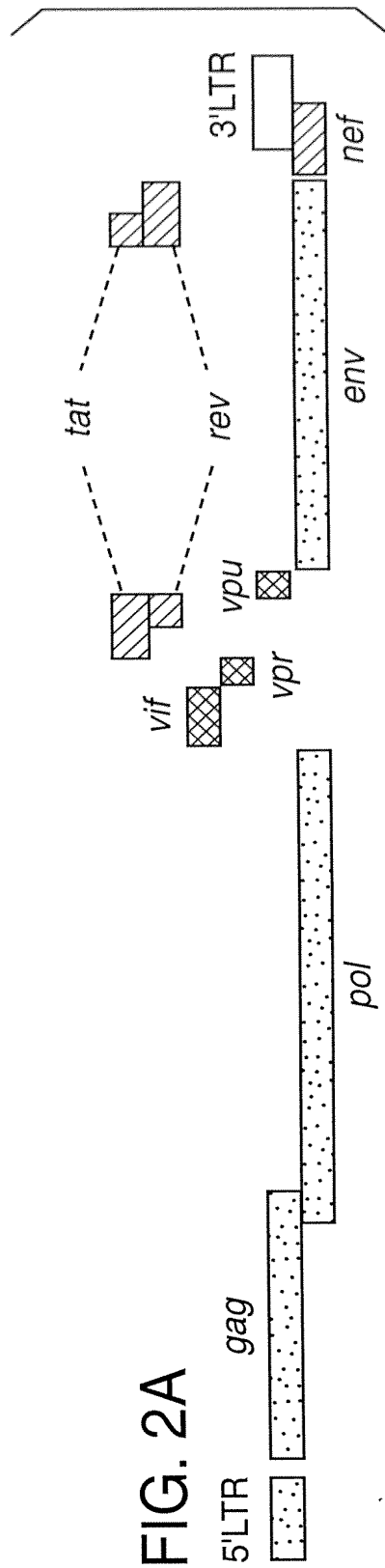


FIG. 2B

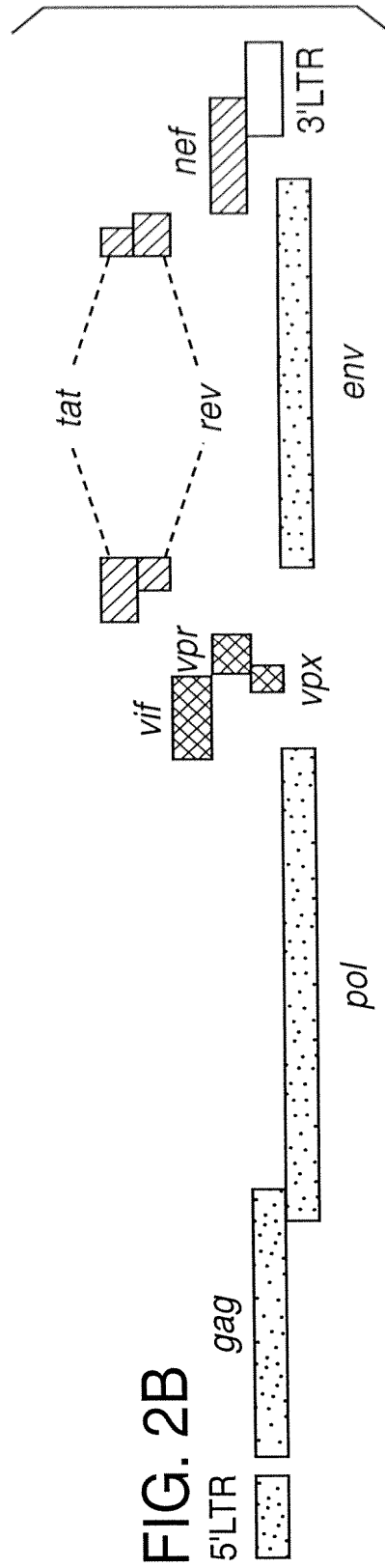


FIG. 3A

pROD(PK36) Leader Sequence

HIV2ROD ROD(PK36)	310	320	330	340	350
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
HIV2ROD ROD(PK36)	360	370	380	390	400
	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
HIV2ROD ROD(PK36)	410	420	430	440	450
	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	GAGCGTGTGG	AGCGGGAGGA
HIV2ROD ROD(PK36)	460	470	480	490	500
	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
	GAAAGAGGCT	CCGGGTGAAG	GTAAGTACCT	ACACC	
HIV2ROD ROD(PK36)	510	520	530	540	550
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
					T GGGAGATGGG

FIG. 3B

pROD(SK36) Leader Sequence

HIV2ROD ROD(SK36)	310	320	330	340	350
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
	GTTGG				
HIV2ROD ROD(SK36)	360	370	380	390	400
	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
HIV2ROD ROD(SK36)	410	420	430	440	450
	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
HIV2ROD ROD(SK36)	460	470	480	490	500
	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
	CT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
HIV2ROD ROD(SK36)	510	520	530	540	550
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG

FIG. 3C

pROD(SD36) Leader Sequence

HIV2ROD ROD(SD36)	310	320	330	340	350
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
	GTTGG				
HIV2ROD ROD(SD36)	360	370	380	390	400
	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
HIV2ROD ROD(SD36)	410	420	430	440	450
	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
HIV2ROD ROD(SD36)	460	470	480	490	500
	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
	CT	CCGGGTGAAG	GTAAGTACCT	ACACC	
HIV2ROD ROD(SD36)	510	520	530	540	550
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
				GT	GGGAGATGGG

FIG. 3D

pROD(CG36) Leader Sequence (Designed and to be created)

HIV2ROD ROD(CG36)	310	320	330	340	350
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
HIV2ROD ROD(CG36)	360	370	380	390	400
	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
	GCTGAGTGAA	GGCAGTAAGG			
HIV2ROD ROD(CG36)	410	420	430	440	450
	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
HIV2ROD ROD(CG36)	460	470	480	490	500
	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
	CT	CCGGGTGAAG	GTAAGTACCT	ACACC	
HIV2ROD ROD(CG36)	510	520	530	540	550
	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
				GT	GGGAGATGGG

FIG. 3E

pROD(MR36) Leader Sequence (Designed and to be created)

HIV2ROD ROD(MR36)	310 GTTGGCGCCT GTTGG	320 GAACAGGGAC	330 TTGAAGAAGA	340 CTGAGAAGTC	350 TTGGAACACG
HIV2ROD ROD(MR36)	360 GCTGAGTGAA	370 GGCAGTAAGG	380 GCGGCAGGAA GCGGCAGGAA	390 CAAACCACGA CAAACCACGA	400 CGGAGTGCTC CGGAGTGCTC
HIV2ROD ROD(MR36)	410 CTAGAAAGGC CTAGAAAGGC	420 GCGGGCCGAG GCGGGCCGAG	430 GTACCAAAGG GTACCAAAGG	440 CAGCGTGTGG GAGCGTGTGG	450 AGCGGGAGGA AGCGGGAGGA
HIV2ROD ROD(MR36)	460 GAAGAGGCCT GAAAGAGGCT	470 CCGGGTGAAG CCGGGTGAAG	480 GTAAGTACCT GTAAGTACCT	490 ACACCAAAAA ACACC	500 CTGTAGCCGA
HIV2ROD ROD(MR36)	510 AAGGGCTTGC	520 TATCCTACCT	530 TTAGACAGGT	540 AGAAGATTGT GT	550 GGGAGATGGG GGGAGATGGG

FIG. 4A

HIV-2 pROD(SD36/EM) Sequence of Mutant Region of Envelope
(Insertion mutant)

ROD	(6351)	ACAGAGGCTT TTGATGCAT	
EM		ACAGAGGCTT TTGATGCATA GGTAGCGTGA GATCTTAGTG CA	
ROD			G GAATAATA CA (6380)
EM		TAGGTAGC GTGAGATCTT AGTGCAAAGA TCGAATAATA CA	

FIG. 4B

pCM-ENV(ROD)(B-14)

```
1   TCAATATTGG CCATTAGCCA TATTATTCAT TGGTTATATA GCATAAATCA
51  ATATTGGCTA TTGGCCATTG CATACTTGT ATCTATATCA TAATATGTAC
101 ATTTATATTG GCTCATGTCC AATATGACCG CCATGTTGGC ATTGATTATT
151 GACTAGTTAT TAATAGTAAT CAATTACGGG GTCATTAGTT CATAGCCCAT
201 ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC GCCTGGCTGA
251 CCGCCCAACG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT
301 AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC
351 GGTAAACTGC CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGTCCG
401 CCCCCATTG ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA
451 GTACATGACC TTACGGGACT TTCTACTTG GCAGTACATC TACGTATTAG
501 TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAC CAATGGGCGT
551 GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC CCATTGACGT
601 CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC
651 GTAATAACCC CGCCCCGTTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG
701 GAGGTCTATA TAAGCAGAGC TCGTTTAGTG AACCGTCAGA TCACTAGAAG
751 CTTTATTGCG GTAGTTTATC ACAGTTAAAT TGCTAACGCA GTCAGTGCTT
801 CTGACACAAC GGTCTCGAAC TTAAGCTGCA GAAGTTGGTC GTGAGGCACT
851 GGGCAGGTAA GTATCAAGGT TACAAGACAG GTTTAAGGAG ACCAATAGAA
901 ACTGGGCTTG TCGAGACAGA GAAGACTCTT GCGTTTCTGA TAGGCACCTA
951 TTGGTCTTAC TGACATCCAC TTTGCCTTTC TCTCCACAGG TGTCCACTCC
1001 CAGTTCAATT ACAGCTCTTA AGGCTAGAGT ACTTAATACG ACTCACTATA
1051 GGCTAGCCTC GA TACACCAGAC AAGTGAGTAT 180
GATGAATCAG CTGCTTATTG CCATTTTATT AGCTAGTGCT TGCTTAGTAT ATTGACCCCA 240
ATATGTAAC TTTTCTATG GCGTACCCAC GTGGAAAAAT GCAACCATTC CCCTCTTTTG 300
310 320 330 340 350 360
TGCAACCAGA AATAGGGATA CTTGGGGAAC CATACTGTC TTGCCTGACA ATGATGATTA 360
TCAGGAAATA ACTTTGAATG TAACAGAGGC TTTTGATGCA TGGAATAATA CAGTAACAGA 420
ACAAGCAATG AAAGATGTCT GGCATCTATT CGAGACATCA ATAAAACCAT GTGTCAAAC 480
AACACCTTTA TGTGTAGCAA TGAAATGCAG CAGCACAGAG AGCAGCATAG GGAACAACAC 540
AACCTCAAAG AGCACAAGCA CAACCACAAC CACACCCACA GACCAGGAGC AAgagataag 600
610 620 630 640 650 660
tgaggatact ccatgcgcac gcgagacaa ctgctcagga ttgggagagg aagaaacgat 660
caattgccag ttcaatatga caggattaga aagagataag aaaaaacagt ataatgaaac 720
atggtactca aaagatgtgg tttgtgagac aaataatagc acaaatcaga cccagtgtta 780
catgaaccat tgcaacacat cagtcacac agaatcatgt gacaagcact attgggatgc 840
tataaggttt agatactgtg caccaccggg ttatgcccta ttaagatgta atgataccaa 900
```

FIG. 4C

910 920 930 940 950 960
ttattcaggc tttgcaccca actgttctaa agtagtagct tctacatgca ccaggatgat 960
ggaaacgcaa acttccacat ggtttggctt taatggcact agagcagaga atagaacata 1020
tatctattgg catggcagag ataatagaac tatcatcagc ttaaacaat attataatct 1080
cagtttgcac tgtaagaggc caggggaataa gatagtgaac caaataatgc ttatgtcagg 1140
acatgtgttt cactcccact accagccgat caataaaaga cccagacaag catggtgctg 1200
1210 1220 1230 1240 1250 1260
gttcaaaggc aaatggaaa acgccatgca ggaggtgaag gaaacccttg caaaacatcc 1260
caggtataga ggaaccaatg acacaaggaa tattagcttt gcagcgccag gaaaaggctc 1320
agaccagaa gtagcataca tgtggactaa ctgcagagga gagtttctct actgcaacat 1380
gacttgggtt ctcaattgga tagagaataa gacacaccgc aattatgcac cgtgccatat 1440
aaagcaaata attaacacat ggcataaggc agggagaaat gtatatttgc ctcccaggga 1500
1510 1520 1530 1540 1550 1560
aggggagctg tcttgcaact caacagtaac cagcataatt gctaacattg actggcaaaa 1560
caataatcag acaaacatta cttttagtgc agaggtggca gaactataca gattggagtt 1620
gggagattat aaattggtag aaataacacc aattggcttc gcacctaca aagaaaaaag 1680
atactcctct gtcacggga gacatacaag aggtgtgttc gtgctagggt tcttgggttt 1740
tctcgcaaca gcaggttctg caatgggcgc ggcgtccctg accgtgtcgg ctccagtcgg 1800
1810 1820 1830 1840 1850 1860
gactttactg gccgggatag tgcagcaaca gcaacagctg ttggacgtgg tcaagagaca 1860
acaagaactg ttgcgactga ccgtctgggg aacgaaaaac ctccaggcaa gagtcactgc 1920
tatagagaag tacctacagg accaggcgcg gctaaattca tggggatgtg cgtttagaca 1980
agtctgccac actactgtac catgggttaa tgattcctta gcacctgact gggacaatat 2040
gacgtggcag gaatgggaaa aacaagtccg ctacctggag gcaaatatca gtaaaagttt 2100
2110 2120 2130 2140 2150 2160
agaacaggca caaattcagc aagagaaaaa tatgtatgaa ctacaaaaat taaatagctg 2160
ggatattttt ggcaattggt ttgacttaac ctcttgggtc aagtatatct aatatggagt 2220
gcttataata gtagcagtaa tagctttaag aatagtgaata tatgtagtac aaatgttaag 2280
taggcttaga aagggtctata ggcctgtttt ctcttccc cccggttata tccaacagat 2340
ccatatccac aaggaccggg gacagccagc caacgaagaa acagaagaag acggtggaag 2400
2410 2420 2430 2440 2450 2460
caacggtgga gacagatact ggccctggcc gatagcaTAT ATACATTTCC TGATCCGCCA 2460
GCTGATTCGC CTCTTGACCA GACTATACAG CATCTGCAGG GACTTACTAT CCAGGAGCTT 2520
CCTGACCCTC CAACTCATCT ACCAGAATCT CAGAGACTGG CTGAGACTTA GAACAGCCTT 2580
CTTGCAATAT GGGTGCGAGT GGATCCAAGA AGCATTCCAG GCCGCCGCGA GGGCTACAAG 2640
AGAGACTCTT GCGGGCGCGT GCAGGGGCTT GTGGAGGGTA TTGGAACGAA TCGGGAGGGG 2700
2710 2720 2730 2740 2750 2760
AATACTCGCG GTTCCAAGAA GGATCAGACA GGGAGCAGAA ATCGCCTCCT GTGAGGGACG 2760
GCAGTATAGC CAGGGAGACT TTATGAATAC TCCATGG

FIG. 4D

GGCGG

1101	CCGCTTCGAG	CAGACATGAT	AAGATACATT	GATGAGTTTG	GACAAACCAC
1151	AACTAGAATG	CAGTGAAAAA	AATGCTTTAT	TTGTGAAATT	TGTGATGCTA
1201	TTGCTTTATT	TGTAACCATT	ATAAGCTGCA	ATAAACAAGT	TAACAACAAC
1251	AATTGCATTC	ATTTTATGTT	TCAGGTTTCAG	GGGGAGATGT	GGGAGGTTTT
1301	TTAAAGCAAG	TAAAACCTCT	ACAAATGTGG	TAAAATCGAT	AAGGATCCGG
1351	GCTGGCGTAA	TAGCGAAGAG	GCCCGCACCG	ATCGCCCTTC	CCAACAGTTG
1401	CGCAGCCTGA	ATGGCGAATG	GACGCGCCCT	GTAGCGGCGC	ATTAAGCGCG
1451	GCGGGTGTGG	TGGTTACGCG	CAGCGTGACC	GCTACACTTG	CCAGCGCCCT
1501	AGCGCCCGCT	CCTTTCGCTT	TCTTCCCTTC	CTTTCTCGCC	ACGTTCGCCG
1551	GCTTTCCCCG	TCAAGCTCTA	AATCGGGGGC	TCCCTTTAGG	GTTCCGATTT

FIG. 4E

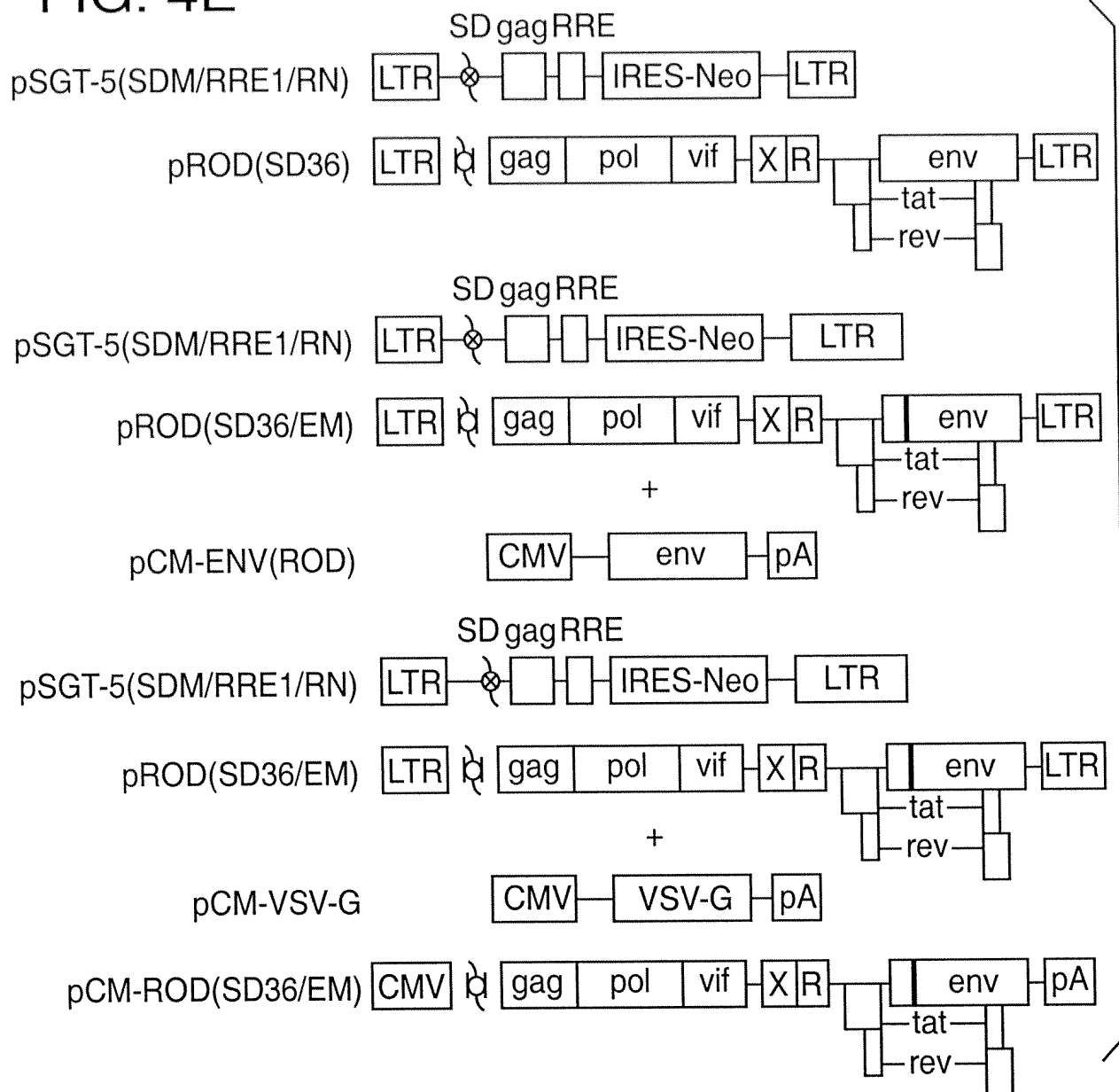


FIG. 5A

SIV 5' LTR Leader Sequence

R→

10	20	30	40	50
GCTCTGTATT	CAGTCGCTCT	GCGGAGAGGC	TGGCAGATTG	AGCCCTGGGA
60	70	80	90	100
GGTTCTCTCC	AGCACTAGCA	GGTAGAGCCT	GGGTGTTCCC	TGCTAGACTC
110	120	130	140	150
TCACCAGCAC	TTGGCCGGTG	CTGGGCAGAG	TGACTCCACG	CTTGCTTGCT
			← R U5 →	
160	170	180	190	200
TAAAGCCCTC	TTCAATAAAG	CTGCCATTTT	AGAAGTAAGC	TAGTGTGTGT
210	220	230	240	250
TCCCATCTCT	CCTAGCCGCC	GCCTGGTCAA	CTCGGTACTC	AATAATAAGA
260	270	280	290	300
AGACCCTGGT	CTGTTAGGAC	CCTTTCTGCT	TTGGGAAACC	GAAGCAGGAA
	← U5 Leader →			
310	320	330	340	350
AATCCCTAGC	AGATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA
360	370	380	390	400
CTCCTGAGTA	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC
410	420	430	440	450
GACGGAGTGC	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG
		SD		
460	470	480	490	500
CGGGAGAGGA	AGAGGCCTCC	GGTTGCAGGT	AAGTGCAACA	CAAAAAAGAA
510	520	530	540	550
ATAGCTGTCT	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG
560				
CGTGAGAAAC				

FIG. 5B

pSIV(SD36)

	320	330	340	350	360
WTL	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
SD36	GATTGG				
	370	380	390	400	410
WTL	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
SD36					
	420	430	440	450	460
WTL	TCCTATAAAG	GCGCGGGTTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
SD36					
	470	SD 480	490	500	510
WTL	AGAGGCCTCC	GGTTGCAGGT	AAGTGCAACA	CAAAAAAGAA	ATAGCTGTCT
SD36	CTCC	GGTTGCAGGT	AAGTGCAACA	CA	
	520	530	540	550	560
WTL	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG	CGTGAGAAAC
SD36			GT	GGGAGATGGG	CGTGAGAAAC

FIG. 5C

pSIV(SDM)

	320	330	340	350	360
WTL	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
SDM	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
	370	380	390	400	410
WTL	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
SDM	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
	420	430	440	450	460
WTL	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
SDM	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
		SD			
	470	480	490	500	510
WTL	AGAGGCCTCC	GGTTGCAGGT	AAGTGCAACA	CAAAAAAGAA	ATAGCTGTCT
SDM	AGAGGCCTCC	GGTTGATATC	GAGTGCAACA	CAAAAAAGAA	ATAGCTGTCT
	520	530	540	550	560
WTL	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG	CGTGAGAAAC
SDM	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAGATGGG	CGTGAGAAAC

FIG. 6A

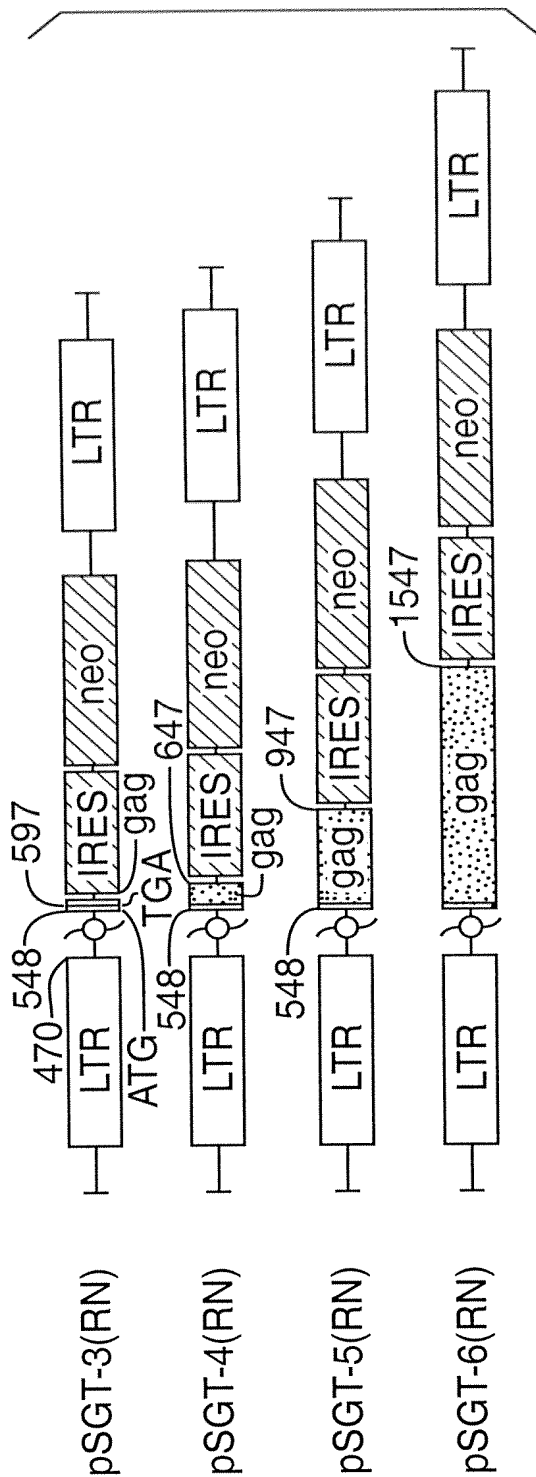


FIG. 6B

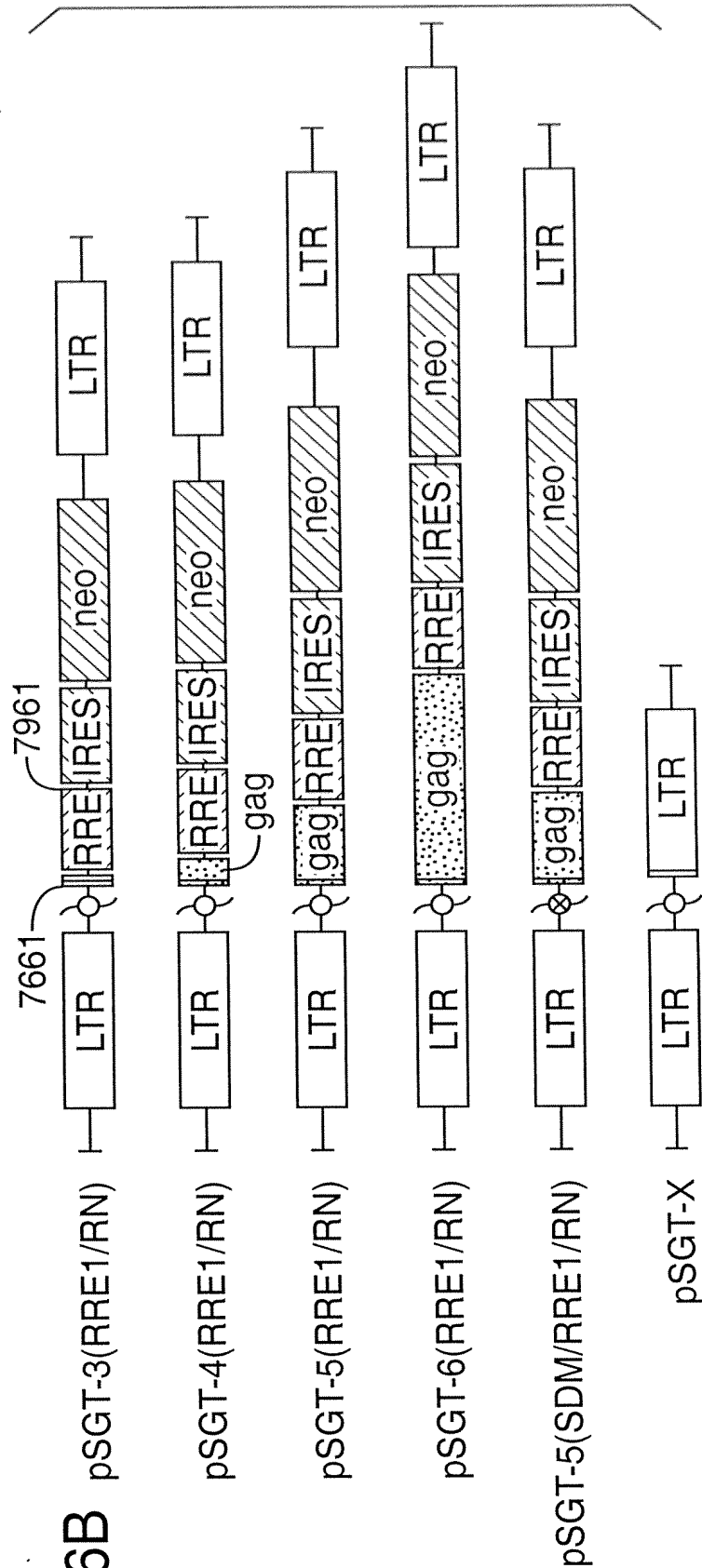


FIG. 7A

pSGT5(SDM/RR)

|U3 -530 -520
GGAA GGGCTGTATT ACAGTGATAG

-530 -520 -510 -500 -490 -480
GAGACGTAGA GTCCTAGACA TATACTTAGA AAAGGAAGAG GGAATAATTG GAGACTGGCA

-470 -460 -450 -440 -430 -420
GAACTATACT CATG GACCAG GAGTAAGGTA TCCAAAGTTC TTTGGGTGGT TATGGAAGCT

-410 -400 -390 -380 -370 -360
AGTACCAGTA GATGTCCCAC AAGA GGGAGA TGACAGTGAG ACTCACTGCT TAGTGCATCC

-350 -340 -330 -320 -310 -300
AGCA CAAACA AGCAGGTTTG ATGACCCGCA TGGAGAAACA TTAGTTTGGA GGTTTGACCC

-290 -280 -270 -260 -250 -240
CACGCTAGCT TTAGCTACG AGGCCTTTAT TCGATACCCA GAGGAGTTTG GGTACAAGTC

-230 -220 -210 -200 -190 -180
AGGCCTGCCA GAGGATGAAT GGAAGGCAAG ACTGAAAGCA AGAGGGATAC CGTTAGCTA

-170 -160 -150 -140 -130 -120
AAAACAGGAA CAGCTATACT TGGTCAGGGC AGGAAGTAAC TAACAGAAAA CAGCTGAGAC

-110 -100 -90 -80 -70 -60
TGCAGGGACT TTCCAGAAGG GGCTGTTACC AGGGGAGGGA CATGGGAGGA GCCGGTGGGG

-50 -40 -30 -20 -10 U3|
AACGCCCTCA TACTTTCTGT ATAAATGTAC CCGCTACTCG CATTGTATTC

|R 10 20 30 40 50 60
GTTTCGCTCTG CGGAGAGGCT GGCAGATTGA GCCCTGGGAG GTTCTCTCCA GCACTAGCAG

70 80 90 100 110 120
TGGTCACCTG GGTGTTCCCT GCTAGACTCT CACCAGTGCT TGGCCGGCAC TGGGCAGACG

130 140 150 160 170 R|U5 180
GCTCCACGCT TGCTTGCTTA AAAGACCTCT TAATAAAGCT GCCAGTTAGA AGCAAGTTAA

190 200 210 220 230 240
GTGTGTGCTC CCATCTCTCC TAGTCGCCGC CTGGTCATTC GGTGTTTCATC TAAAGTAACA

250 260 270 280 290 300
AGACCCTGGT CTGTTAGGAC CCTTTCTGCT TTGGGAAACC AAGGCAGGAA AATCCCTAGC

U5|Leader 310 320 330 340 350 360
AGGTTGGCGC CCGAACAGGG ACTTGAAGAA GACTGAGAAG CTTTGAACA CGGCTGAGTG

370 380 390 400 410 420
AAGGCAGTAA GGGCGGCAGG AACAAACCAC GACGGAGTGC TCCTAGAAAA GCGCAGGCCG

FIG. 7B

430 440 450 460 470|---SDM---| 480
AGGTACCAAG GCGGGCGTGT GGAGCGGGAG TGAAAGAGGC CTCCGGGTGA TATCAGTGCC

490 500 510 520 530 540
TACACCAAAT ACAGTAGCCA GAAGGGCTTG TTATCCTACC TTTAGACGGG TAGAAGATTG

Leader |gag 560 570 580 590 600
TGGGAGATGC CATGGTAGGG CGCGAGAAAC TCCGTCTTGA GAGGGAAAAA AGCAGACGAA

610 620 630 640 650 660
TTAGAAAAGA TTAGGTTACG GCCCGGCGGA AAGAAAAAAT ATAGGCTAAA ACATATTGTG

670 680 690 700 710 720
TGGGCAGCGA ATGAATTGGA CAGATTCGGA TTGGCAGAGA GCCTGTTGGA GTCAAAAGAG

730 740 750 760 770 780
GGTTGCCAAAA AAATTCTTAC AGTTT TAGAT CCATTAGTAC CGACAGGGTC AGAAAATTTA

790 800 810 820 830 840
AAAAGCCTTT TTAATACTGT CTGCGTCATT TGGTGTATAC ACGCAGAAGA GAAAGCGAAA

850 860 870 880 890 900
GATACTGAAG AAGCAAAACA AAAGGTACAG AGACATCTAG TGGCAGAAAC AAAA ACTACA

910 920 930 940 950gag(955) |poly(L)
GAAAAAATGC CAAGTACAAG TAGACCAACA GCACCACCTA GCGGGAACGG AGGAACTCGA

970 980 |RRE(7661) 990 1000 1010 1020
ATGCATGGTG ACCGCGGCCG CAGAGGTGTA TTCGTGCTAG GGTTCCTTAGG TTTTCTCACA

1030 1040 1050 1060 1070 1080
GCAGGAGCTG CAATGGGCGC GGCGTCCTTG ACGCTGTCGG CTCAGTCTCG GACTTTATTG

1090 1100 1110 1120 1130 1140
GCCGGGATAG TGCAGCAACA GCAACAGCTG TTGGACGTGG TCAAGAGACA ACAAGAAATG

1150 1160 1170 1180 1190 1200
TTGCGACTGA CCGTCTGGGG AACAAAAAAT CTCCAGGCAA GAGTCACTGC TATCGAGAAA

1210 1220 1230 1240 1250 1260
TACTTAAAGG ACCAGGCGC AACTAAATTCA TGGGGATGTG CGTCTAGACA AGTCTGCCAC

1270 RRE(7960)| poly(L) 1290 |(8770) 1310 1320
ACTACTGTAC CATGGGTAGC GGCCGCTCGC GAGTAGACCA TGGAGAGCCC CAGCAGAAGG

1330 1340 1350 1360 1370 1380
GGAGAAAGGC TCGTACAAGC AACAAAAATAT GGATGATGTA GATTCAAGATG ATGATGACCT

1390 1400 1410 1420 1430 1440
AGTAGGGGTC CCTGTCACAC CAAGAGTACC ATTAAGAGAA ATGACATATA GGTGGCAAG

1450 1460 1470 (8944)|U3 1480 1490 1500
AGAT ATGTCA CATTTGATAA AAGAAAAGGG GGGACTGGAA GGGCTGTATT ACAGTGATAG

FIG. 7C

1510 1520 1530 1540 1550 1560
GAGACGTAGA GTCCTAGACA TATACTTAGA AAAGGAAGAG GGAATAATTG GAGACTGGCA

1570 1580 1590 1600 1610 1620
GAACTATACT CATG GACCAG GAGTAAGGTA TCCAAAGTTC TTTGGGTGGT TATGGAAGCT

1630 1640 1650 1660 1670 1680
AGTACCAGTA GATGTCCCAC AAGA GGGAGA TGACAGTGAG ACTCACTGCT TAGTGCATCC

1690 1700 1710 1720 1730 1740
AGCA CAAACA AGCAGGTTTG ATGACCCGCA TGGAGAAACA TTAGTTTGGA GGTTTGACCC

1750 1760 1770 1780 1790 1800
CACGCTAGCT TTAGCTACG AGGCCTTTAT TCGATACCCA GAGGAGTTTG GGTACAAGTC

1810 1820 1830 1840 1850 1860
AGGCCTGCCA GAGGATGAAT GGAAGGCAAG ACTGAAAGCA AGAGGGATAC CGTTAGCTA

1870 1880 1890 1900 1910 1920
AAAACAGGAA CAGCTATACT TGGTCAGGGC AGGAAGTAAC TAACAGAAAA CAGCTGAGAC

1930 1940 1950 1960 1970 1980
TGCAGGGACT TTCCAGAAGG GGCTGTTACC AGGGGAGGGA CATGGGAGGA GCCGGTGGGG

1990 2000 2010 2020 U3|R 2040
AACGCCCTCA TACTTTCTGT ATAAATGTAC CCGCTACTCG CATTGTATTC AGTCGCTCTG

2050 2060 2070 2080 2090 2100
CGGAGAGGCT GGCAGATTGA GCCC TGGGAG GTTCTCTCCA GCACTAGCAG GTAGGCCTG

2110 2120 2130 2140 2150 2160
GGTGTTCCCT GCTAGACTCT CACCAGTGCT TGGCCGGCAC TGGGCAGACG GCTCCACGCT

2170 2180 2190 R|
TGCTTGCTTA AAAGACCTCT TAATAAAGC TGCCA

FIG. 7D

10	20	30	40	50	60
TCTAGAGGAA	TTCCGCCCCCT	CTCCCTCCCC	CCCCCCTAAC	GTTACTGGCC	GAAGCCGCTT
70	80	90	100	110	120
GGAATAAGGC	CGGTGTGCGT	TTGTCTATAT	GTTATTTTCC	ACCATATTGC	CGTCTTTTGG
130	140	150	160	170	180
CAATGTGAGG	GCCCGGAAAC	CTGGCCCTGT	CTTCTTGACG	AGCATTCTTA	GGGGTCTTTC
190	200	210	220	230	240
CCCTCTCGCC	AAAGGAATGC	AAGGTCTGTT	GAATGTCGTG	AAGGAAGCAG	TTCTCTGGA
250	260	270	280	290	300
AGCTTCTTGA	AGACAAACAA	CGTCTGTAGC	GACCCCTTTC	AGGCAGCGGA	ACCCCCCACC
310	320	330	340	350	360
TGGCGACAGG	TGCCTCTGCG	GCCAAAAGCC	ACGTGTATAA	GATACACCTG	CAAAGGCGGC
370	380	390	400	410	420
ACAACCCAG	TGCCACGTTG	TGAGTTGGAT	AGTTGTGGAA	AGAGTCAAAT	GGCTCTCCTC
430	440	450	460	470	480
AAGCGTATTC	AACAAGGGGC	TGAAGGATGC	CCAGAAGGTA	CCCCATTGTA	TGGGATCTGA
490	500	510	520	530	540
TCTGGGGCCT	CGGTGCACAT	GCTTTACATG	TGTTTAGTCG	AGGTTAAAAA	ACGTCTAGGC
550	560	570	580	590	600
CCCCCGAACC	ACGGGGACGT	GGTTTTCTCT	TGAAAAACAC	GATGATAAGC	TTGCCACAAC
610	620	630	640	650	660
CATGGCTGAA	CAAGATGGAT	TGCACGCAGG	TTCTCCGGCC	GCTTGGGTGG	AGAGGCTATT
670	680	690	700	710	720
CGGCTATGAC	TGGGCACAAC	AGACAATCGG	CTGCTCTGAT	GCCGCCGTGT	TCCGGCTGTC
730	740	750	760	770	780
AGCGCAGGGG	CGCCCGGTTC	TTTTTGTCAA	GACCGACCTG	TCCGGTGCCC	TGAATGAACT
790	800	810	820	830	840
GCAGGACGAG	GCAGCGCGGC	TATCGTGGCT	GGCCACGACG	GGCGTTCTCT	GCGCAGCTGT
850	860	870	880	890	900
GCTCGACGTT	GTCACTGAAG	CGGGAAGGGA	CTGGCTGCTA	TTGGGCGAAG	TGCCGGGGCA
910	920	930	940	950	960
GGATCTCCTG	TCATCTCACC	TTGCTCCTGC	CGAGAAAGTA	TCCATCATGG	CTGATGCAAT
970	980	990	1000	1010	1020
GCGGCGGCTG	CATACGCTTG	ATCCGGCTAC	CTGCCCATTG	GACCACCAAG	CGAAACATCG
1030	1040	1050	1060	1070	1080
CATCGAGCGA	GCACGTACTC	GGATGGAAGC	CGGTCTTGTC	GATCAGGATG	ATCTGGACGA
1090	1100	1110	1120	1130	1140
AGAGCATCAG	GGGCTCGCGC	CAGCCGAAC	GTTTCGCCAGG	CTCAAGGCGC	GCATGCCCCA
1150	1160	1170	1180	1190	1200
CGGCGAGGAT	CTCGTCGTGA	CCCATGGCGA	TGCCTGCTTG	CCGAATATCA	TGGTGGAAAA
1210	1220	1230	1240	1250	1260
TGGCCGCTTT	TCTGGATTCA	TCGACTGTGG	CCGGCTGGGT	GTGGCGGACC	GCTATCAGGA
1270	1280	1290	1300	1310	1320
CATAGCGTTG	GCTACCCGTG	ATATTGCTGA	AGAGCTTGGC	GGCGAATGGG	CTGACCGCTT
1330	1340	1350	1360	1370	1380
CCTCGTGCTT	TACGGTATCG	CCGCTCCCGA	TTCGCAGCGC	ATCGCCTTCT	ATCGCCTTCT
1390	1400	1410			
TGACGAGTTC	TTCTGAGCGG	GATCGGCTAG	C		

FIG. 7E

pSGT-5(SDM) 5'LTR-Leader Sequence

	10	20	30	40	50
HIV2ST	GTTCGCTCTG	CGGAGAGGCT	GGCAGATTGA	GCCCTGGGAG	GTTCTCTCCA
pSGT5(SDM)	GTTCGCTCTG	CGGAGAGGCT	GGCAGATTGA	GCCCTGGGAG	GTTCTCTCCA
	60	70	80	90	100
HIV2ST	GCACTAGCAG	TGGTCACCTG	GGTGTTCCCT	GCTAGACTCT	CACCAGTGCT
pSGT5(SDM)	GCACTAGCAG	TGGTCACCTG	GGTGTTCCCT	GCTAGACTCT	CACCAGTGCT
	110	120	130	140	150
HIV2ST	TGGCCGGCAC	TGGGCAGACG	GCTCCACGCT	TGCTTGCTTA	AAAGACCTCT
pSGT5(SDM)	TGGCCGGCAC	TGGGCAGACG	GCTCCACGCT	TGCTTGCTTA	AAAGACCTCT
	160	170	180	190	200
HIV2ST	TAATAAAGCT	GCCAGTTAGA	AGCAAGTTAA	GTGTGTGCTC	CCATCTCTCC
pSGT5(SDM)	TAATAAAGCT	GCCAGTTAGA	AGCAAGTTAA	GTGTGTGCTC	CCATCTCTCC
	210	220	230	240	250
HIV2ST	TAGTCGCCGC	CTGGTCATTC	GGTGTTTCATC	TAAAGTAACA	AGACCCTGGT
pSGT5(SDM)	TAGTCGCCGC	CTGGTCATTC	GGTGTTTCATC	TAAAGTAACA	AGACCCTGGT
	260	270	280	290	300
HIV2ST	CTGTTAGGAC	CCTTTCTGCT	TTGGGAAACC	AAGGCAGGAA	AATCCCTAGC
pSGT5(SDM)	CTGTTAGGAC	CCTTTCTGCT	TTGGGAAACC	AAGGCAGGAA	AATCCCTAGC
	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
pSGT5(SDM)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDM)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDM)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
	460	470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	AGGTAAGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDM)	TGAAAGAGGC	CTCCGGGTGA	TATC AGTGC	CTACACCAAA	TACAGTAGCC
	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDM)	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 7F

pSGT-5(SDM) Leader Sequence

	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
pSGT5(SDM)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDM)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDM)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
		SD			
	460	470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	AGGTA AGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDM)	TGAAAGAGGC	CTCCGGGTGA	TATC AGTGC	CTACACCAAA	TACAGTAGCC
	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDM)	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 7G

pSGT-5(SDX) Leader Sequence

	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
pSGT5(SDX)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDX)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDX)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
		SD			
	460	470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	AGGTAAGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDX)	TGAAAGAGGC	CTCCGG	GC	CTACACCAAA	TACAGTAGCC
	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDX)	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 8

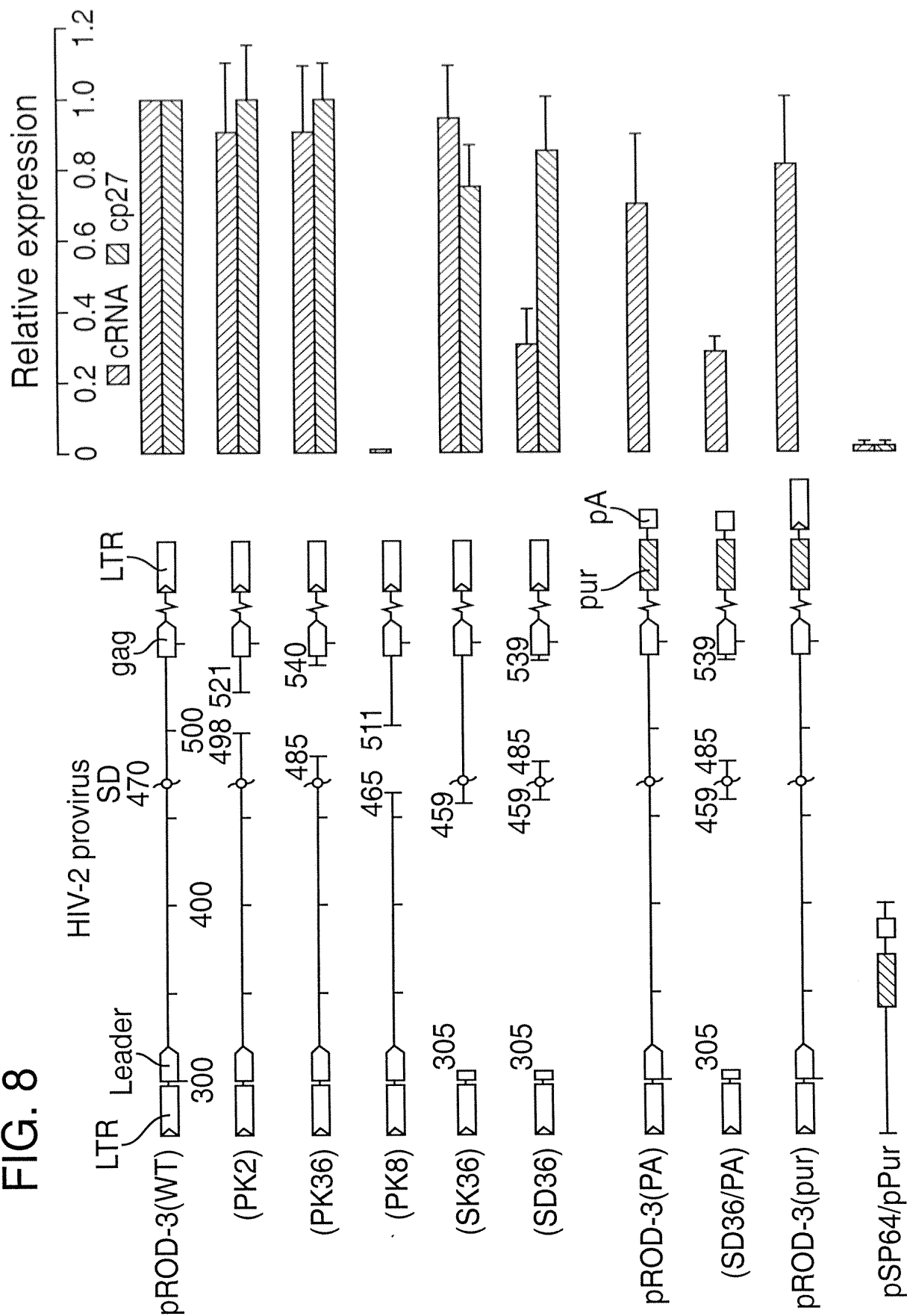


FIG. 9

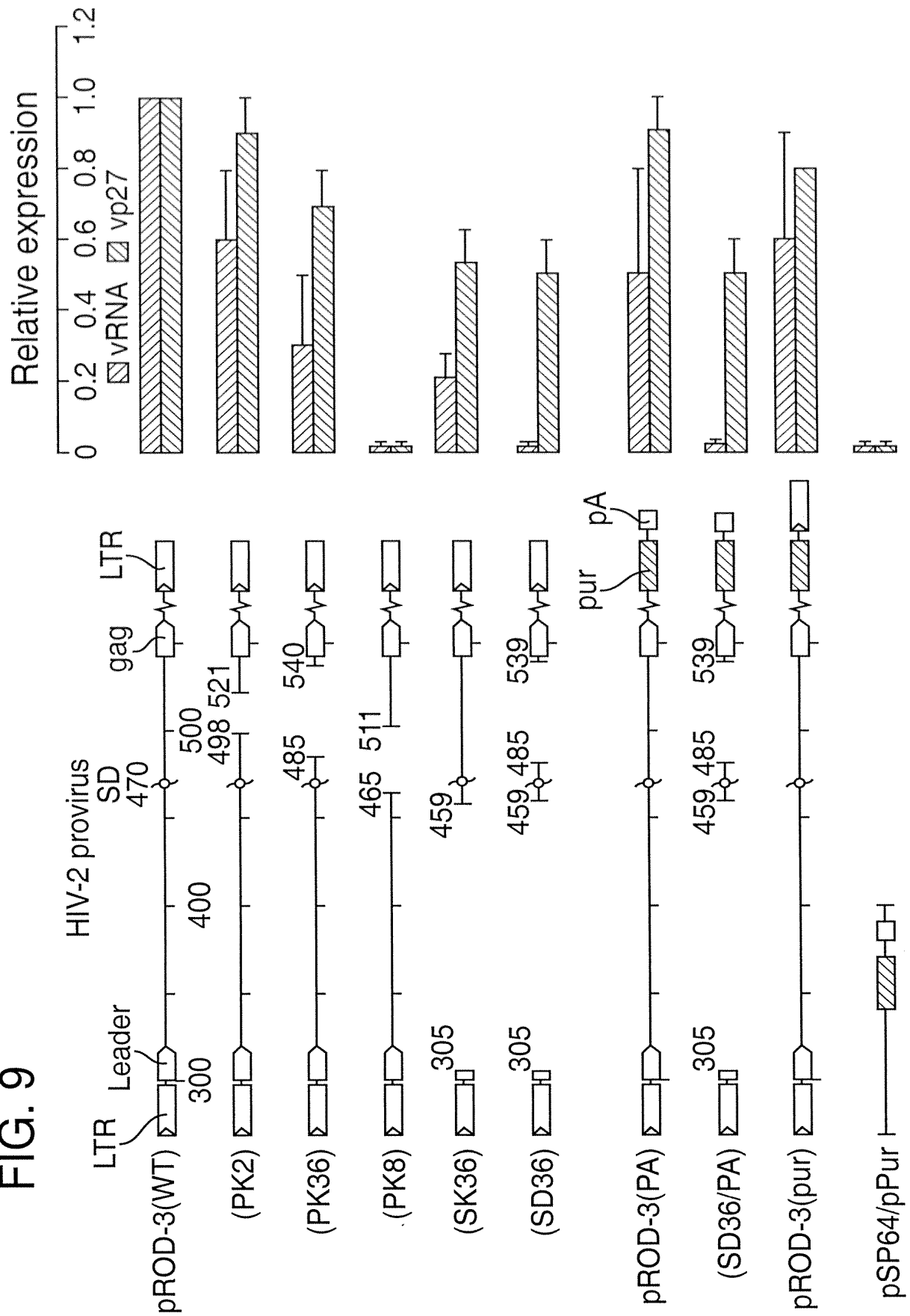
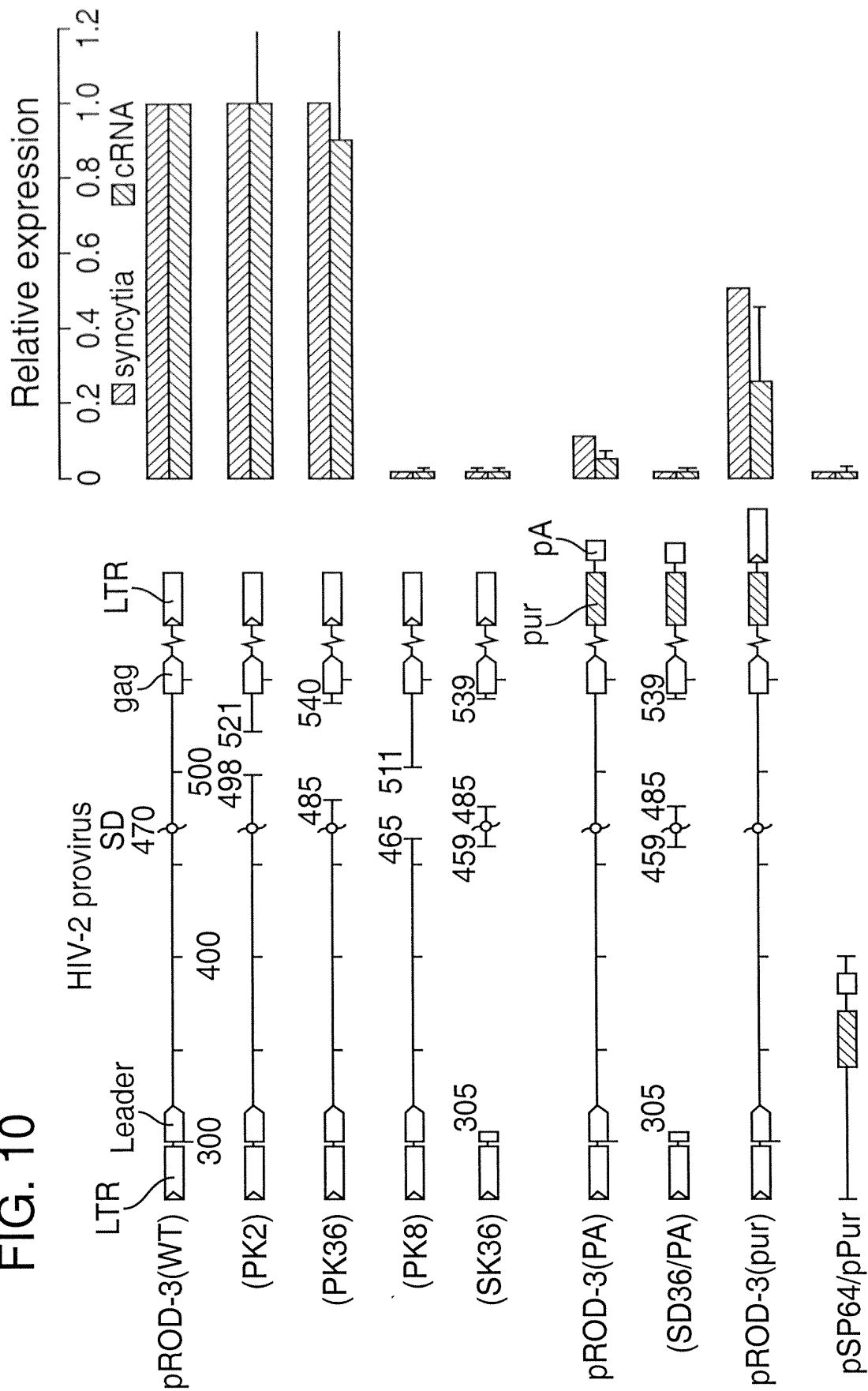
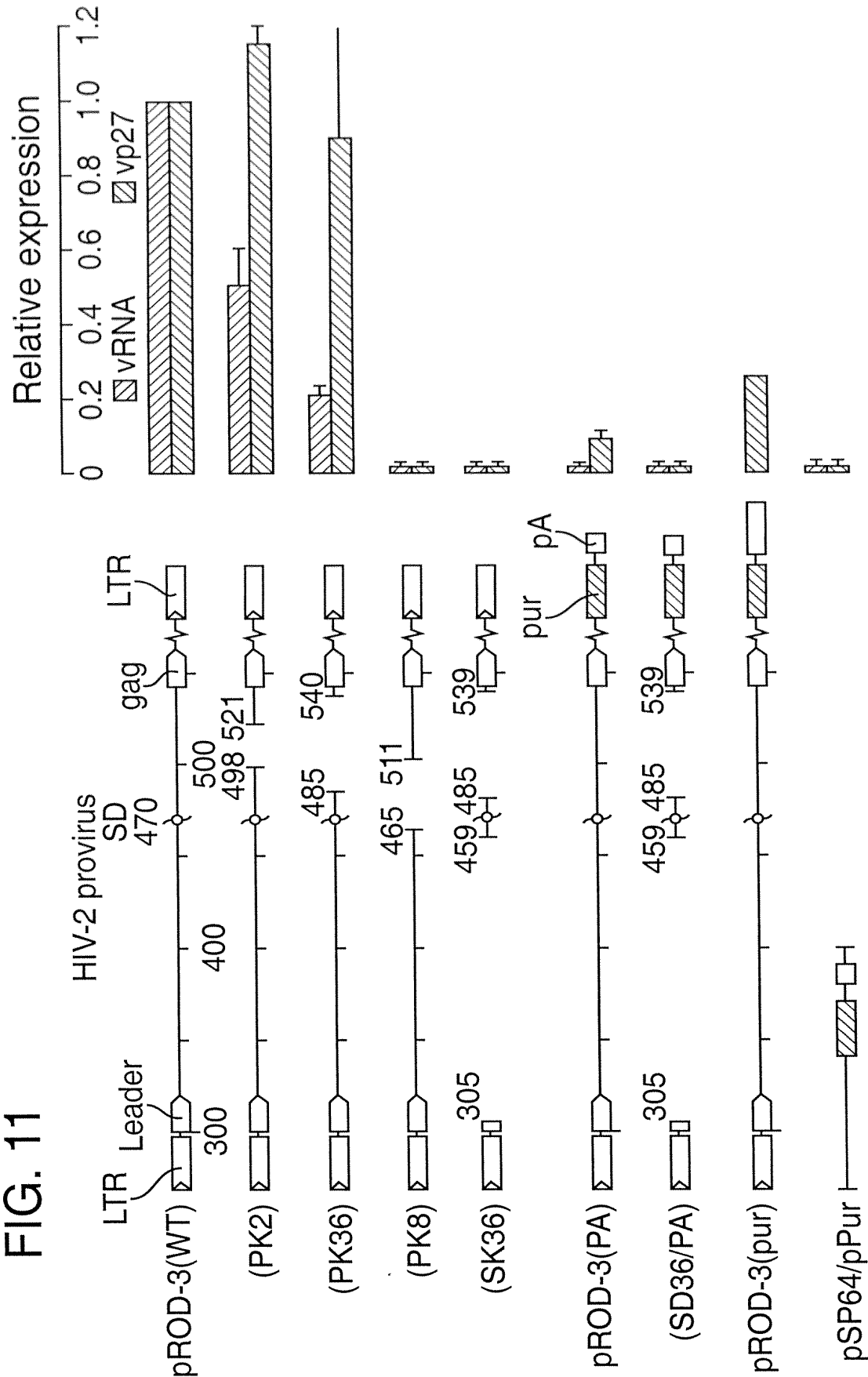


FIG. 10





HIV-2 Lentivirus: Gene Transfer Models

FIG. 14

